

Karaolis1.ST25.txt
SEQUENCE LISTING

<110> KARAOLIS, David K.R.

<120> METHOD FOR ATTENUATING VIRULENCE OF MICROBIAL PATHOGENS AND FOR INHIBITING MICROBIAL BIOFILM FORMATION

<130> KARAOLIS1 PCT

<140> NOT YET ASSIGNED

<141> 2004-07-22

<150> 60/490,029

<151> 2003-07-25

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 2055

<212> DNA

<213> V. cholerae

<220>

<221> CDS

<222> (1)..(2055)

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acg tca cac agt ccg ttc ttt ttt gca atc ctc aat gat caa cac caa	96
Thr Ser His Ser Pro Phe Phe Phe Ala Ile Leu Asn Asp Gln His Gln	
20 25 30	
tac gtg atg gtc aac gag cgc tat tgt gat atc gcc ggt ctc tct agc	144
Tyr Val Met Val Asn Glu Arg Tyr Cys Asp Ile Ala Gly Leu Ser Ser	
35 40 45	
gaa gag atg gtc ggg atg agc gat agt cag gtt ctg ggc gaa cat ttt	192
Glu Glu Met Val Gly Met Ser Asp Ser Gln Val Leu Gly Glu His Phe	
50 55 60	
tat cgc cat ctc aaa ccg ttt tac gaa cgt gcg ttt aac aac gag cat	240
Tyr Arg His Leu Lys Pro Phe Tyr Glu Arg Ala Phe Asn Asn Glu His	
65 70 75 80	
att gag tcc gag ctg acc ctc agc gaa atc gac ctc gaa acc agc tta	288
Ile Glu Ser Glu Leu Thr Leu Ser Glu Ile Asp Leu Glu Thr Ser Leu	
85 90 95	
cac ttt tct ctc tcc ccc atc atg atc aac gat cgg gtg caa tac ctt	336
His Phe Ser Leu Ser Pro Ile Met Ile Asn Asp Arg Val Gln Tyr Leu	
100 105 110	
gta ttc cac gcg att gat acc tca gaa aag cag att tta gtg cgc tct	384
Val Phe His Ala Ile Asp Thr Ser Glu Lys Gln Ile Leu Val Arg Ser	
115 120 125	
ctg gaa gaa tcg gaa agc aaa tac gca ctc ctc acg aca ctg cta cct	432
Leu Glu Glu Ser Glu Ser Lys Tyr Ala Leu Leu Thr Thr Leu Leu Pro	
130 135 140	
gat ggt tta atg atg gtg gaa aat gac tgc att att tct gcc aac cct	480
Asp Gly Leu Met Met Val Glu Asn Asp Cys Ile Ile Ser Ala Asn Pro	

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145	150	155	160	
tcc gct gca cgt tta ctc ggt ttt gac gac gca caa aaa ctg ctc gga Ser Ala Ala Arg Leu Leu Gly Phe Asp Asp Ala Gln Lys Leu Leu Gly	165	170	175	528
gaa aat ctc tcc aga ctg ttt att gat gaa aag acc aaa acc gtt ttt Glu Asn Leu Ser Arg Leu Phe Ile Asp Glu Lys Thr Lys Thr Val Phe	180	185	190	576
tca tcg cag ttg gct tcg cta ctg aca gaa aaa ccc ttg gtg tgc ttg Ser Ser Gln Leu Ala Ser Leu Leu Thr Glu Lys Pro Leu Val Cys Leu	195	200	205	624
acc ggg cca agg tgt ggg ttt gaa cgg aaa atc cag tta cac gca ggt Thr Gly Pro Arg Cys Gly Phe Glu Arg Lys Ile Gln Leu His Ala Gly	210	215	220	672
tgc acc tct tta ctc ggt aat cag tcg cag ttg atc tta ttg caa gat Cys Thr Ser Leu Leu Gly Asn Gln Ser Gln Leu Ile Leu Leu Gln Asp	225	230	235	720
gcc gat gaa gcc cca aaa cag ttt tct gcg acc act caa gtc gat gcg Ala Asp Glu Ala Pro Lys Gln Phe Ser Ala Thr Thr Gln Val Asp Ala	245	250	255	768
cat att gat agc ctc act ggg ctg tat aac cga cac ggg ttt acc aag His Ile Asp Ser Leu Thr Gly Leu Tyr Asn Arg His Gly Phe Thr Lys	260	265	270	816
cgc tta gag cag tgc atc caa aat gag acg cct ttg gtt atg ctc tat Arg Leu Glu Gln Cys Ile Gln Asn Glu Thr Pro Leu Val Met Leu Tyr	275	280	285	864
ctg gac att gat aac ttc aaa aac atc aat gac tct ctc ggc cat cac Leu Asp Ile Asp Asn Phe Lys Asn Ile Asn Asp Ser Leu Gly His His	290	295	300	912
atc ggt gac aaa gtg att aaa gag gtg gcg gca cgt tta aaa cgc tta Ile Gly Asp Lys Val Ile Lys Glu Val Ala Ala Arg Leu Lys Arg Leu	305	310	315	960
ctg cca cag caa gcc gta ctt ggc cat ttg ggc ggt gat gag ttt ggt Leu Pro Gln Gln Ala Val Leu Gly His Leu Gly Gly Asp Glu Phe Gly	325	330	335	1008
ttg atc ttg ccg gag cca gaa cac aac cgc tct gca gaa atg ttg gca Leu Ile Leu Pro Glu Pro Glu His Asn Arg Ser Ala Glu Met Leu Ala	340	345	350	1056
gat cgc att atc tct ttg att aat cag cct ttt gac ctg cac cat ttc Asp Arg Ile Ile Ser Leu Ile Asn Gln Pro Phe Asp Leu His His Phe	355	360	365	1104
agt aag cgt tta gct tgt tcg att ggc agc gtg cgt tat ccc ggt gac Ser Lys Arg Leu Ala Cys Ser Ile Gly Ser Val Arg Tyr Pro Gly Asp	370	375	380	1152
ggc aat gat gct cgc gta tta ctg caa aat gcc gat acc gcg atg tat Gly Asn Asp Ala Arg Val Leu Leu Gln Asn Ala Asp Thr Ala Met Tyr	385	390	395	1200
gag gct aaa gag cgc ggt cgc aat cgc ctg atc aaa ttc aat gat cag Glu Ala Lys Glu Arg Gly Arg Asn Arg Leu Ile Lys Phe Asn Asp Gln	405	410	415	1248
atg aac aaa gaa gcg cgg atg cgc ctt tgg ttg gaa att gaa ctg caa Met Asn Lys Glu Ala Arg Met Arg Leu Trp Leu Glu Ile Glu Leu Gln				1296

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420								425		430						
aaa Lys	gcg Ala	cta Leu 435	caa Gln	caa Gln	aac Asn	ggc Gly	cta Leu 440	gaa Glu	gtg Val	tgg Trp	tac Tyr	caa Gln 445	ccg Pro	aaa Lys	gtc Val	1344
aac Asn	gcg Ala 450	cgt Arg	gat Asp	ttt Phe	agc Ser	atc Ile 455	aat Asn	ggc Gly	gca Ala	gaa Glu	gcc Ala 460	ttg Leu	gta Val	cgc Arg	tgg Trp	1392
aaa Lys 465	cat His	ccc Pro	gtt Val	gaa Glu	ggc Gly 470	tat Tyr	atc Ile	agc Ser	cca Pro	ggt Gly 475	gct Ala	ttc Phe	att Ile	ccc Pro	gtt Val 480	1440
gcg Ala	gaa Glu	aaa Lys	gcc Ala	ggc Gly 485	tta Leu	atc Ile	gaa Glu	cat His	ttg Leu 490	ggt Gly	cgc Arg	gtg Val	gtt Val	atg Met 495	cgt Arg	1488
gaa Glu	gtc Val	ttc Phe	gcg Ala 500	acc Thr	gtc Val	aag Lys	cgc Arg	tgg Trp 505	aag Lys	cta Leu	caa Gln	ggc Gly	att Ile 510	tta Leu	ccc Pro	1536
gga Gly	cgt Arg	gtg Val 515	gcg Ala	atc Ile	aac Asn	atc Ile	tcc Ser 520	ccc Pro	gag Glu	cag Gln	ttt Phe	ggc Gly 525	aat Asn	cct Pro	caa Gln	1584
ctg Leu	att Ile 530	gat Asp	tat Tyr	tta Leu	gaa Glu	aaa Lys 535	cta Leu	ctg Leu	cga Arg	aca Thr	act Thr 540	ggg Gly	cta Leu	gat Asp	ccc Pro	1632
aac Asn 545	aac Asn	atc Ile	aca Thr	ttt Phe	gaa Glu 550	ctg Leu	acc Thr	gaa Glu	agt Ser	gtg Val 555	gtg Val	atg Met	agc Ser	gat Asp	agt Ser 560	1680
gaa Glu	cat His	acc Thr	cag Gln	caa Gln 565	atg Met	ctc Leu	aat Asn	gcc Ala	atc Ile 570	aag Lys	aaa Lys	ctc Leu	ggc Gly	ttc Phe 575	acc Thr	1728
ttg Leu	tca Ser	att Ile	gat Asp 580	gac Asp	ttc Phe	ggt Gly	aca Thr	ggt Gly 585	tac Tyr	tcg Ser	tcg Ser	ctg Leu	gct Ala 590	tat Tyr	tta Leu	1776
gct Ala	cgc Arg	ttc Phe 595	ccg Pro	atc Ile	gat Asp	gag Glu	ctc Leu 600	aaa Lys	atc Ile	gac Asp	cgc Arg	gcg Ala 605	ttt Phe	atc Ile	agt Ser	1824
aat Asn	atc Ile 610	gac Asp	act Thr	cta Leu	ccc Pro	aaa Lys 615	cag Gln	ctc Leu	acg Thr	gtg Val	att Ile 620	gaa Glu	aac Asn	atc Ile	att Ile	1872
aat Asn 625	ttg Leu	ggg Gly	cgc Arg	tca Ser	ctg Leu 630	aac Asn	ctg Leu	acc Thr	gta Val	gtt Val 635	gca Ala	gaa Glu	gga Gly	gta Val	gaa Glu 640	1920
act Thr	cag Gln	caa Gln	caa Gln	gcc Ala 645	act Thr	tta Leu	ctc Leu	tcc Ser	aac Asn 650	cta Leu	aat Asn	tgc Cys	cac His	tcc Ser 655	atc Ile	1968
caa Gln	ggc Gly	ttc Phe	cat His 660	ttt Phe	tat Tyr	cgc Arg	cca Pro	caa Gln 665	ccg Pro	aag Lys	cac His	gaa Glu	gtg Val 670	gaa Glu	gag Glu	2016
ttg Leu	ttt Phe	gcg Ala 675	caa Gln	aat Asn	cgc Arg	cgc Arg	cat His 680	cgc Arg	aaa Lys	tcc Ser	ctc Leu	taa				2055

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<211> 684

<212> PRT

<213> V. cholerae

<400> 2

Met Pro Ala Gln Thr Ser Ser Gln Leu Lys His Trp Phe Ala Lys Ile
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Tyr Val Met Val Asn Glu Arg Tyr Cys Asp Ile Ala Gly Leu Ser Ser
 35 40 45

Glu Glu Met Val Gly Met Ser Asp Ser Gln Val Leu Gly Glu His Phe
 50 55 60

Tyr Arg His Leu Lys Pro Phe Tyr Glu Arg Ala Phe Asn Asn Glu His
 65 70 75 80

Ile Glu Ser Glu Leu Thr Leu Ser Glu Ile Asp Leu Glu Thr Ser Leu
 85 90 95

His Phe Ser Leu Ser Pro Ile Met Ile Asn Asp Arg Val Gln Tyr Leu
 100 105 110

Val Phe His Ala Ile Asp Thr Ser Glu Lys Gln Ile Leu Val Arg Ser
 115 120 125

Leu Glu Glu Ser Glu Ser Lys Tyr Ala Leu Leu Thr Thr Leu Leu Pro
 130 135 140

Asp Gly Leu Met Met Val Glu Asn Asp Cys Ile Ile Ser Ala Asn Pro
 145 150 155 160

Ser Ala Ala Arg Leu Leu Gly Phe Asp Asp Ala Gln Lys Leu Leu Gly
 165 170 175

Glu Asn Leu Ser Arg Leu Phe Ile Asp Glu Lys Thr Lys Thr Val Phe
 180 185 190

Ser Ser Gln Leu Ala Ser Leu Leu Thr Glu Lys Pro Leu Val Cys Leu
 195 200 205

Thr Gly Pro Arg Cys Gly Phe Glu Arg Lys Ile Gln Leu His Ala Gly
 210 215 220

Cys Thr Ser Leu Leu Gly Asn Gln Ser Gln Leu Ile Leu Leu Gln Asp
 225 230 235 240

Ala Asp Glu Ala Pro Lys Gln Phe Ser Ala Thr Thr Gln Val Asp Ala
 245 250 255

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His Ile Asp Ser Leu Thr Gly Leu Tyr Asn Arg His Gly Phe Thr Lys
 260 265 270
 Arg Leu Glu Gln Cys Ile Gln Asn Glu Thr Pro Leu Val Met Leu Tyr
 275 280 285
 Leu Asp Ile Asp Asn Phe Lys Asn Ile Asn Asp Ser Leu Gly His His
 290 295 300
 Ile Gly Asp Lys Val Ile Lys Glu Val Ala Ala Arg Leu Lys Arg Leu
 305 310 315 320
 Leu Pro Gln Gln Ala Val Leu Gly His Leu Gly Gly Asp Glu Phe Gly
 325 330 335
 Leu Ile Leu Pro Glu Pro Glu His Asn Arg Ser Ala Glu Met Leu Ala
 340 345 350
 Asp Arg Ile Ile Ser Leu Ile Asn Gln Pro Phe Asp Leu His His Phe
 355 360 365
 Ser Lys Arg Leu Ala Cys Ser Ile Gly Ser Val Arg Tyr Pro Gly Asp
 370 375 380
 Gly Asn Asp Ala Arg Val Leu Leu Gln Asn Ala Asp Thr Ala Met Tyr
 385 390 395 400
 Glu Ala Lys Glu Arg Gly Arg Asn Arg Leu Ile Lys Phe Asn Asp Gln
 405 410 415
 Met Asn Lys Glu Ala Arg Met Arg Leu Trp Leu Glu Ile Glu Leu Gln
 420 425 430
 Lys Ala Leu Gln Gln Asn Gly Leu Glu Val Trp Tyr Gln Pro Lys Val
 435 440 445
 Asn Ala Arg Asp Phe Ser Ile Asn Gly Ala Glu Ala Leu Val Arg Trp
 450 455 460
 Lys His Pro Val Glu Gly Tyr Ile Ser Pro Gly Ala Phe Ile Pro Val
 465 470 475 480
 Ala Glu Lys Ala Gly Leu Ile Glu His Leu Gly Arg Val Val Met Arg
 485 490 495
 Glu Val Phe Ala Thr Val Lys Arg Trp Lys Leu Gln Gly Ile Leu Pro
 500 505 510
 Gly Arg Val Ala Ile Asn Ile Ser Pro Glu Gln Phe Gly Asn Pro Gln
 515 520 525

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Leu Ile Asp Tyr Leu Glu Lys Leu Leu Arg Thr Thr Gly Leu Asp Pro
 530 535 540
 Asn Asn Ile Thr Phe Glu Leu Thr Glu Ser Val Val Met Ser Asp Ser
 545 550 555 560
 Glu His Thr Gln Gln Met Leu Asn Ala Ile Lys Lys Leu Gly Phe Thr
 565 570 575
 Leu Ser Ile Asp Asp Phe Gly Thr Gly Tyr Ser Ser Leu Ala Tyr Leu
 580 585 590
 Ala Arg Phe Pro Ile Asp Glu Leu Lys Ile Asp Arg Ala Phe Ile Ser
 595 600 605
 Asn Ile Asp Thr Leu Pro Lys Gln Leu Thr Val Ile Glu Asn Ile Ile
 610 615 620
 Asn Leu Gly Arg Ser Leu Asn Leu Thr Val Val Ala Glu Gly Val Glu
 625 630 635 640
 Thr Gln Gln Gln Ala Thr Leu Leu Ser Asn Leu Asn Cys His Ser Ile
 645 650 655
 Gln Gly Phe His Phe Tyr Arg Pro Gln Pro Lys His Glu Val Glu Glu
 660 665 670
 Leu Phe Ala Gln Asn Arg Arg His Arg Lys Ser Leu
 675 680

<210> 3
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 <213> Artificial

<220>
 <223> synthetic

<400> 3
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31

<210> 4
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 <212> DNA
 <213> Artificial

<220>
 <223> synthetic

<400> 4
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29

<210> 5
 <211> 5

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<212> PRT
<213> Artificial

<220>
<223> synthetic

<220>
<221> misc_feature
<222> (3)..(3)
<223> Residue at this position can be either Asp or Glu.

<400> 5

Gly Gly Xaa Glu Phe
1 5